

(FILE 'HOME' ENTERED AT 09:40:38 ON 05 MAY 2005)

FILE 'AGRICOLA, MEDLINE, CAPLUS, BIOSIS' ENTERED AT 09:40:41 ON 05 MAY 2005

L1	2 S VERSICOLOR AND (PYRF OR (OROTATE (2N) TRANSFERASE))
L2	2 DUP REM L1 (0 DUPLICATES REMOVED)
L3	0 S VERSICOLOR AND TRASFERASE
L4	18 S VERSICOLOR AND TRANSFERASE
L5	14 DUP REM L4 (4 DUPLICATES REMOVED)
L6	11 S L5 AND PY<2000

Database :       A\_Geneseq\_16Dec04:\*

1:   geneseqp1980s:\*

2:   geneseqp1990s:\*

3:   geneseqp2000s:\*

4:   geneseqp2001s:\*

5:   geneseqp2002s:\*

6:   geneseqp2003as:\*

7:   geneseqp2003bs:\*

8:   geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result		%					
No.	Score	Query	Match	Length	DB	ID	Description
1	1158	100.0	227	4	AAB46894		Aab46894 T. versic
2	504.5	43.6	216	6	ABU16739		Abu16739 Protein e
3	504.5	43.6	247	6	ADA33758		Ada33758 Acinetoba
4	458	39.6	213	6	ABU38902		Abu38902 Protein e
5	458	39.6	222	7	ABO75095		Abo75095 Pseudomon
6	458	39.6	277	7	ABO64083		Abo64083 Klebsiell
7	453	39.1	213	4	AAB75103		Aab75103 E. coli o
8	453	39.1	213	6	ABU28822		Abu28822 Protein e
9	452	39.0	214	6	ABU49061		Abu49061 Protein e
10	451	38.9	213	6	ABU31219		Abu31219 Protein e
11	451	38.9	215	6	ABU50113		Abu50113 Protein e
12	446	38.5	213	6	ABU45257		Abu45257 Protein e
13	446	38.5	213	6	ABU48380		Abu48380 Protein e
14	439	37.9	213	6	ABU28226		Abu28226 Protein e
15	438	37.8	246	8	ADR86103		Adr86103 Aspergill

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	504.5	43.6	247	4	US-09-328-352-5045	Sequence 5045, Ap
2	458	39.6	222	4	US-09-252-991A-23841	Sequence 23841, A
3	458	39.6	277	4	US-09-489-039A-10600	Sequence 10600, A
4	414	35.8	201	4	US-09-543-681A-7516	Sequence 7516, Ap
5	395.5	34.2	211	4	US-09-248-796A-18107	Sequence 18107, A
6	230.5	19.9	443	4	US-09-675-018B-12	Sequence 12, Appl
7	207.5	17.9	476	4	US-09-675-018B-13	Sequence 13, Appl
8	207.5	17.9	476	4	US-09-675-018B-14	Sequence 14, Appl
9	203	17.5	478	4	US-09-675-018B-6	Sequence 6, Appli
10	197.5	17.1	476	4	US-09-675-018B-8	Sequence 8, Appli
11	197.5	17.1	476	4	US-09-675-018B-10	Sequence 10, Appl
12	165.5	14.3	210	4	US-09-583-110-2852	Sequence 2852, Ap
13	162.5	14.0	211	4	US-09-107-532A-5221	Sequence 5221, Ap
14	160.5	13.9	257	4	US-09-134-000C-6094	Sequence 6094, Ap

Database :       Published\_Applications\_AA:\*

- 1:   /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*
- 2:   /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3:   /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
- 4:   /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*
- 5:   /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*
- 6:   /cgn2\_6/ptodata/2/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7:   /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*
- 8:   /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB.pep:\*
- 9:   /cgn2\_6/ptodata/2/pubpaa/US09A\_PUBCOMB.pep:\*
- 10:  /cgn2\_6/ptodata/2/pubpaa/US09B\_PUBCOMB.pep:\*
- 11:  /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep:\*
- 12:  /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*
- 13:  /cgn2\_6/ptodata/2/pubpaa/US10A\_PUBCOMB.pep:\*
- 14:  /cgn2\_6/ptodata/2/pubpaa/US10B\_PUBCOMB.pep:\*
- 15:  /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep:\*
- 16:  /cgn2\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep:\*
- 17:  /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*
- 18:  /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*
- 19:  /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*
- 20:  /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	504.5	43.6	216	15	US-10-282-122A-44663	Sequence 44663, A
2	458	39.6	213	15	US-10-282-122A-66826	Sequence 66826, A
3	453	39.1	213	15	US-10-282-122A-56746	Sequence 56746, A
4	452	39.0	214	15	US-10-282-122A-76985	Sequence 76985, A
5	451	38.9	213	15	US-10-282-122A-59143	Sequence 59143, A
6	451	38.9	215	15	US-10-282-122A-78037	Sequence 78037, A
7	446	38.5	213	15	US-10-282-122A-73181	Sequence 73181, A
8	446	38.5	213	15	US-10-282-122A-76304	Sequence 76304, A
9	439	37.9	213	15	US-10-282-122A-56150	Sequence 56150, A

Database :       PIR\_79:\*  
               1:  pir1:\*  
               2:  pir2:\*  
               3:  pir3:\*  
               4:  pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	485	41.9	225	2	A36459	orotate phosphorib
2	462.5	39.9	226	1	XJBY5	orotate phosphorib
3	458	39.6	213	2	A82981	orotate phosphorib
4	454	39.2	213	2	S32801	orotate phosphorib
5	453	39.1	213	1	XJEC	orotate phosphorib
6	452	39.0	213	2	F86040	orotate phosphorib
7	452	39.0	213	2	E91193	orotate phosphorib
8	452	39.0	214	2	E82350	orotate phosphorib
9	451	38.9	215	2	AF0006	orotate phosphorib
10	449	38.8	233	1	S30118	orotate phosphorib
11	446	38.5	213	2	AH0970	orotate phosphorib
12	446	38.5	215	2	T40667	orotate phosphorib
13	432	37.3	213	2	I64058	orotate phosphorib
14	428.5	37.0	227	1	XJBY10	orotate phosphorib
15	428.5	37.0	232	1	JS0175	orotate phosphorib
16	426	36.8	219	2	S55840	orotate phosphorib
17	422.5	36.5	213	2	H81032	probable orotate p
18	416.5	36.0	231	1	A29459	orotate phosphorib

Database : UniProt\_03:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	516.5	44.6	244	2	O74686	O74686 ajellomyces
2	499.5	43.1	237	2	Q6F6Z6	Q6f6z6 acinetobact
3	490	42.3	225	2	Q870L6	Q870l6 cryptococcu
4	486	42.0	225	2	Q870L7	Q870l7 cryptococcu
5	485	41.9	225	1	PYRE_CRYNE	P18132 cryptococcu
6	485	41.9	225	2	Q71BG6	Q71bg6 cryptococcu
7	485	41.9	225	2	Q870L8	Q870l8 cryptococcu
8	484	41.8	225	2	O13404	O13404 cryptococcu
9	484	41.8	225	2	Q70Q41	Q70q41 cryptococcu
10	482	41.6	225	2	Q92230	Q92230 cryptococcu
11	479	41.4	225	2	O13405	O13405 cryptococcu
12	478	41.3	225	2	O13406	O13406 cryptococcu
13	477	41.2	225	2	Q92232	Q92232 cryptococcu
14	477	41.2	225	2	Q86ZQ7	Q86zq7 cryptococcu
15	474	40.9	225	2	Q870L9	Q870l9 cryptococcu
16	473.5	40.9	224	2	Q00524	Q00524 cryptococcu
17	473	40.8	225	2	Q92231	Q92231 cryptococcu
18	472	40.8	218	2	O13487	O13487 mucor circi
19	465	40.2	208	2	Q9UW68	Q9uw68 cryptococcu
20	465	40.2	210	2	Q9UW60	Q9uw60 cryptococcu
21	465	40.2	211	2	Q9UQW8	Q9uqw8 cryptococcu
22	464	40.1	210	2	Q9UQZ3	Q9uqz3 cryptococcu
23	464	40.1	215	1	PYRE_SHEON	Q8e915 shewanella
24	464	40.1	223	2	Q6FP51	Q6fp51 candida gla
25	462.5	39.9	226	1	PYRE_YEAST	P13298 saccharomyc

Database : GenEmbl:\*  
 1: gb\_ba:\*  
 2: gb\_htg:\*  
 3: gb\_in:\*  
 4: gb\_om:\*  
 5: gb\_ov:\*  
 6: gb\_pat:\*  
 7: gb\_ph:\*  
 8: gb\_pl:\*  
 9: gb\_pr:\*  
 10: gb\_ro:\*  
 11: gb\_sts:\*  
 12: gb\_sy:\*  
 13: gb\_un:\*  
 14: gb\_vi:\*

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#### SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	3448	100.0	3448	6	AX078057	AX078057 Sequence
	2	613	17.8	684	6	AX078058	AX078058 Sequence
	3	132.4	3.8	877	8	S47907	S47907 PYR1=orotat
c	4	131.6	3.8	11175	1	AE014701	AE014701 Bifidobac
c	5	131.6	3.8	349980	6	AX492784	AX492784 Sequence
c	6	131.6	3.8	349980	6	AX553951	AX553951 Sequence
	7	131.2	3.8	642	12	AY657552	AY657552 Synthetic
c	8	131.2	3.8	3123	1	PAU38241	U38241 Pseudomonas
c	9	131.2	3.8	10384	1	AE004945	AE004945 Pseudomon
	10	126.6	3.7	313518	1	AE016856	AE016856 Pseudomon

Database : N\_Geneseq\_16Dec04:\*

- 1: geneseqn1980s:\*
- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			%		Query		DB	ID	Description
	No.	Score	Match	Length					
	1	3448	100.0	3448	4	AAF26441			Aaf26441 T. versic
	2	613	17.8	684	4	AAF26442			Aaf26442 T. versic
	3	132.8	3.9	669	11	ABD08666			Abd08666 Pseudomon
c	4	132.8	3.9	780	11	ABD08827			Abd08827 Pseudomon
c	5	131.6	3.8	349980	6	ABQ81846			Abq81846 Bifidobac
	6	131.2	3.8	642	8	ACA42772			Aca42772 Prokaryot
	7	130.2	3.8	522	11	ABD08602			Abd08602 Pseudomon
	8	120.6	3.5	642	8	ACA52250			Aca52250 Prokaryot
	9	120.4	3.5	639	8	ACA49127			Aca49127 Prokaryot
	10	113.8	3.3	639	8	ACA32096			Aca32096 Prokaryot



Database : Issued Patents NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

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#### SUMMARIES

Result			% Query		DB	ID	Description
	No.	Score	Match	Length			
c	1	132.8	3.9	669	4	US-09-252-991A-7270	Sequence 7270, Ap
	2	132.8	3.9	780	4	US-09-252-991A-7431	Sequence 7431, Ap
	3	130.2	3.8	522	4	US-09-252-991A-7206	Sequence 7206, Ap
	4	109	3.2	744	4	US-09-328-352-919	Sequence 919, Appl
	5	107.2	3.1	834	4	US-09-489-039A-3429	Sequence 3429, Ap
c	6	104.4	3.0	405	4	US-09-252-991A-7491	Sequence 7491, Ap
	7	89	2.6	31063	4	US-09-596-002-20	Sequence 20, Appl
c	8	82.4	2.4	7218	1	US-08-232-463-14	Sequence 14, Appl
	9	72.8	2.1	3238	4	US-09-949-016-5546	Sequence 5546, Ap
	10	72.8	2.1	9300	4	US-09-949-016-12482	Sequence 12482, A
	11	72.8	2.1	9301	4	US-09-949-016-17288	Sequence 17288, A
	12	72.2	2.1	152132	4	US-09-949-016-13845	Sequence 13845, A
	13	72.2	2.1	152145	4	US-09-949-016-12371	Sequence 12371, A
	14	71.8	2.1	1926	3	US-09-249-585A-2	Sequence 2, Appli
	15	71.8	2.1	1926	4	US-09-410-399-3	Sequence 3, Appli
	16	71.8	2.1	2580	3	US-09-050-863-2	Sequence 2, Appli

Database :           Published\_Applications\_NA:\*

- 1:   /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2:   /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3:   /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4:   /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5:   /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6:   /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7:   /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8:   /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9:   /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
- 10:  /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11:  /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
- 12:  /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*
- 13:  /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*
- 14:  /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15:  /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 16:  /cgn2\_6/ptodata/2/pubpna/US10D\_PUBCOMB.seq:\*
- 17:  /cgn2\_6/ptodata/2/pubpna/US10E\_PUBCOMB.seq:\*
- 18:  /cgn2\_6/ptodata/2/pubpna/US10F\_PUBCOMB.seq:\*
- 19:  /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*
- 20:  /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 21:  /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 22:  /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

		%					Description
Result	Query	Match	Length	DB	ID		
No.	Score						
c	1	131.6	3.8	2256646	18	US-10-470-565-1	Sequence 1, Appli
	2	131.2	3.8	642	17	US-10-282-122A-30642	Sequence 30642, A
	3	120.6	3.5	642	17	US-10-282-122A-40120	Sequence 40120, A
	4	120.4	3.5	639	17	US-10-282-122A-36997	Sequence 36997, A
	5	113.8	3.3	639	17	US-10-282-122A-19966	Sequence 19966, A
	6	106.8	3.1	639	17	US-10-282-122A-22959	Sequence 22959, A
	7	99.4	2.9	648	17	US-10-282-122A-8479	Sequence 8479, Ap
	8	97	2.8	1578	10	US-09-834-434-1	Sequence 1, Appli
	9	96.4	2.8	642	17	US-10-282-122A-20562	Sequence 20562, A
	10	92.2	2.7	645	17	US-10-282-122A-40801	Sequence 40801, A
	11	89	2.6	582	17	US-10-282-122A-26975	Sequence 26975, A
	12	89	2.6	31063	17	US-10-672-787-20	Sequence 20, Appl

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_htc:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result			%					
No.	Score	Match	Length	DB	ID		Description	
c 1	121.4	3.5	682	7	CF932870		CF932870 TrEST-B21	
c 2	114	3.3	506	6	CD293012		CD293012 StrPu536.	
c 3	112.8	3.3	532	7	CO423261		CO423261 GGEZHT101	
c 4	112.8	3.3	827	7	CN822809		CN822809 Oa_splbn_	
c 5	112.8	3.3	834	7	CN822771		CN822771 Oa_splbn_	
c 6	110.6	3.2	819	7	CO202239		CO202239 Oa_splbn_	
c 7	110.6	3.2	832	7	CN824810		CN824810 Oa_splbn_	
8	104.2	3.0	632	6	CD486120		CD486120 CFUS6.2F0	
9	103.6	3.0	284	4	BM868752		BM868752 mgns001xN	
c 10	98.2	2.8	1661	9	AG435089		AG435089 Mus muscu	
11	91.4	2.7	616	6	CB826279		CB826279 rw23d06.y	
c 12	87.8	2.5	1168	4	BM468388		BM468388 AGENCOURT	
13	86.6	2.5	751	8	BZ570207		BZ570207 msh2_1230	